

Genome version 5.1.4.15.4578  
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OR nucleotide nucleotide search, using sw model

Run on: March 2, 2003, 13:52:59 ; Search time 11329 seconds  
(without alignment)  
11827.109 Million cell updates/sec  
Filter: us-10-000-213-3  
Refined score: 4604  
Sequences: 1 query:us-10-000-213-3

Search table: 168N11Y\_NP

Gapop 10.0 ; Gapop 1.0

Sequences: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum hit seq length: 0

Maximum hit seq length: 26999999

Post processing: Minimum Match 100%

Maximum Match 100%

Listing First 45 Summaries

Database :

1: db\_1a1a\*  
2: db\_1a1a\*  
3: db\_1a1a\*  
4: db\_1a1a\*  
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41: db\_1a1a\*  
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43: db\_1a1a\*  
44: db\_1a1a\*  
45: db\_1a1a\*

Note: No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4604	100.0	4604	9	HUMVDR
2	4463.4	75.2	3466	9	AB002168 Homo sapi
3	4223.4	70.0	122186	6	AB002168 Homo sapi
4	4223.4	70.0	122186	6	AB002168 Homo sapi
5	4219	69.9	194109	2	AC121438 Homo sapi
6	1573.4	34.2	1687	9	AB024840 Homo sapi
7	1343.4	25.0	1345	9	AB024840 Homo sapi
8	1284	27.9	1284	9	AB024840 Homo sapi
9	1282.4	27.9	1284	6	AB024840 Homo sapi
10	1213.4	25.4	1284	9	AB024840 Homo sapi
11	1114	25.1	2043	10	AB024840 Homo sapi
12	1112	24.2	3428	10	AB024840 Homo sapi
13	1011.4	22.0	1377	10	AB024840 Homo sapi
14	966.4	21.0	1131	6	AB024840 Homo sapi
15	911.4	19.8	1404	6	AB024840 Homo sapi
16	799.4	17.4	2494	5	AB024840 Homo sapi
17	779.2	16.9	1071	6	AB024840 Homo sapi
18	771.6	16.8	1724	5	AB024840 Homo sapi
19	654.6	14.2	2429	5	AB024840 Homo sapi
20	637.4	13.8	780	6	AB024840 Homo sapi
21	634.4	13.8	762	6	AB024840 Homo sapi
22	633.8	13.8	1503	5	AB024840 Homo sapi
23	618.6	13.4	2659	5	AB024840 Homo sapi
24	575.8	12.5	1782	5	AB024840 Homo sapi
25	494.2	10.7	972	5	AB024840 Homo sapi
26	487.2	10.6	2169	6	AB024840 Homo sapi
27	354.2	7.9	911	6	AB024840 Homo sapi
28	356	7.7	380	6	AB024840 Homo sapi
29	350.6	7.6	197631	2	AB024840 Homo sapi
30	345.8	7.5	199484	2	AB024840 Homo sapi
31	298.6	6.5	645	5	AB024840 Homo sapi
32	281	6.1	164203	2	AB024840 Homo sapi
33	272.8	5.9	1305	6	AB024840 Homo sapi
34	272.8	5.9	1374	6	AB024840 Homo sapi
35	272.8	5.9	1422	6	AB024840 Homo sapi
36	272.8	5.9	2020	9	AB024840 Homo sapi
37	272.8	5.9	2145	6	AB024840 Homo sapi
38	272.8	5.9	2146	9	AB024840 Homo sapi
39	272.8	5.9	2803	9	AB024840 Homo sapi
40	272.8	5.9	2905	9	AB024840 Homo sapi
41	272.8	5.9	3057	6	AB024840 Homo sapi
42	272.8	5.9	3243	6	AB024840 Homo sapi
43	270	5.9	2727	9	AB024840 Homo sapi
44	269.6	5.9	4448	9	AB024840 Homo sapi
45	261.8	5.7	1305	9	AB024840 Homo sapi

# ALIGNMENTS

RESULT 1

HUMVDR	HUMVDR	4604 bp	mkna	linear	PR1 14-JAN-1996
DEFINITION	Human vitamin D receptor mRNA, complete cds.				
ACCESSION	J04258				
VERSION	J04258.1	GI:40202			
KEYWORDS	vitamin D receptor,				
SOURCE	Human jejunum, cDNA to mRNA, clones lambda VDR [1,2] and VDR-3.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 4604)				
AUTHORS	Baker, A.R., McDonnell, D.P., Budhes, M., Crisp, J.M., Mamelet, D., Haussler, M.R., Pike, J.W., Shine, J., and O'Malley, B.W.				



































[illegible]























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Db 3841 CTGAGTTTAACTCCATCAAGGCTATATAGAAAGAGAGAGATCACTCTGCGTC 3900
QY 3901 AATGGAAACACAGCTATCTATATATATATATATATATATATATATATATAT 3960
Db 3901 AATGGAAACACAGCTATCTATATATATATATATATATATATATATATATAT 3960
QY 3961 GCTTGTGATAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4020
Db 3961 GCTTGTGATAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4020
QY 4021 TTCTGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4080
Db 4021 TTCTGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4080
QY 4081 CCTGGGCGGCGACACACACACACACACACACACACACACACACACACACAC 4140
Db 4081 CCTGGGCGGCGACACACACACACACACACACACACACACACACACACACAC 4140
QY 4141 AAAAAAGGAGAAATGATATTTTATGCGGCTGCAATGCGGCTGCAATGCGG 4200
Db 4141 AAAAAAGGAGAAATGATATTTTATGCGGCTGCAATGCGGCTGCAATGCGG 4200
QY 4201 TACTTACATGACAGCTGTGAAATAGACATTTTAAATGAAATTTTAAAGTAT 4260
Db 4201 TACTTACATGACAGCTGTGAAATAGACATTTTAAATGAAATTTTAAAGTAT 4260
QY 4261 TATAACTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4320
Db 4261 TATAACTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4320
QY 4321 GAAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4380
Db 4321 GAAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4380
QY 4381 GAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4440
Db 4381 GAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4440
QY 4441 AACAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4500
Db 4441 AACAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4500
QY 4501 AACCAATGATGAAAGCTTTTATGTAATGTAATGTAATGTAATGTAATGTA 4560
Db 4501 AACCAATGATGAAAGCTTTTATGTAATGTAATGTAATGTAATGTAATGTA 4560
QY 4561 CTTTCTGCAAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4604
Db 4561 CTTTCTGCAAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4604

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RESULT 2

AAV41427

ID AAV41327 strand1, DNA, 4604 bp.

XX AC AAV41327;

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XX AC AAV41327;

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XX 23-JUL-1998.
PD 22-DEC-1997; 97WC-US22974.
XX 27-MAY-1997; 97US-0048309.
PR 16-JAN-1997; 97NS-0035382.
XX (UNMA-) UNIV MARYLAND BALTIMORE.
PA (UNPJ-) UNIV PITTSBURGH.
XX Ferrell RE, Hagberg JM;
DR WPI; 1998-414128/35.
XX P-PSDR; AAW68156.
XX Analysis of genetic markers to identify subjects who will benefit
PT from exercise also assessing risk of cardiovascular disease from
PI angiotensin converting enzyme genotype
XX Disclosure; Page 49-53; 61pp; English.
XX This is the human vitamin D receptor gene that codes for a protein
CC (see AAW68156) that plays a central role in the regulation of calcium
CC metabolism, and hence in determining bone homeostasis. The
CC receptor has a polymorphic variation that is detected with BsmI.
CC There are 3 associated genotypes, bb, Bb, and BB, that are related
CC to circulating osteocalcin levels and bone mineral density in both
CC young and postmenopausal women. A claimed method comprises
CC identifying individuals having a certain phenotype, determining the
CC presence or absence of genetic markers associated with the
CC phenotype, and instituting a lifestyle change to exploit or
CC counteract the phenotype expressed by the gene marker. If the
CC phenotype is a reduction of bone mineral density, the gene marker
CC is the vitamin D receptor and exercise training is instituted to
CC increase bone mineral density. The general method can be used to
CC identify subjects who will benefit most from physical exercise and
CC also to identify those who are likely to be successful in sports.
XX Sequence 4604 BP, 1114 A, 1279 C, 1196 G, 1015 T, 0 other;
SQ

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Query Match 100.0%; Score 4602.4; DB 19; Length 4604;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4603; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGAACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAG 60
Db 1 GGAACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAG 60
QY 61 AGCTCAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 120
Db 61 AGCTCAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 120
QY 121 GGAACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 121 GGAACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 181 GATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGA 240
Db 181 GATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGA 240
QY 241 GATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGA 300
Db 241 GATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGA 300
QY 301 CAACGGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCA 360
Db 301 CAACGGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCA 360
QY 361 AGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGA 420
Db 361 AGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGA 420

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Vitamin D receptor gene

Vitamin D receptor gene

Vitamin D receptor gene

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Db 49528 AGGCTGAACTAATAGACTTACCTTG-TTGGAACTACTGCTGAAATAAATGCTTT 49586
QY 49596 ATGTAAGAAAT 4604
Db 49587 ATGTAAGAAAT 49595

RESULT 5
AAQ51424
Db AAQ51424 standard: cDNA; 1399 bp.
XX
Aa AAQ51424:
Db 16 MAY-1994 (first entry)
XX
Human vitamin D receptor coding sequence.
XX
1,25-dihydroxyvitamin D4 receptor; recombinant protein production;
KW insect host; ds.
XX homo sapiens.
XX OS 255260199 A.
XX DN
XX PD
XX PF 30-JUL-1991; 910S-0747746.
XX PR 30-JUL-1991; 910S-0747736.
XX TA (WISN) WISCONSIN ALUMNI RES FOUND.
XX PI DeJura HP, Pradl JM, Reiss IK;
XX WR 1994 467874/46.
XX
Recombinant produ. of 1,25-dihydroxy-vitamin D3 receptor protein
PI using expression system comprising insect cell host and
PI recombinant virus contg. foreign DNA
XX Dislosures: Columns 13-16; 13pp; English.
XX
The 1,25-dihydroxyvitamin D3 receptor is recombinantly produced
XX using insect host cells transformed with DNA coding for an animal
XX (pred. human, rat, porcine or avian) vitamin D receptor. The coding
XX sequence is incorporated into a recombinant baculovirus vector for
XX transfection of the insect host, the human version of the coding
XX sequence was published in Baker et al., Proc. Natl. Acad. Sci USA 85;
XX 6294-6298 (1988).
XX
Sequence 1399 bp; 412 A; 445 C; 470 G; 282 T; 0 other;
SQ
Query Match 40.4%; Score 1397.4; DB 14; Length 1399;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1398; Conserved 1; Indels 0; Gaps 0;

QY 1 GGAAGATTTGGTACGCGGCGGCGGACCAAGGCTTTGAGTCGAGGCGTGTGAG 60
Db 1 GGAAGATTTGGTACGCGGCGGCGGACCAAGGCTTTGAGTCGAGGCGTGTGAG 60
QY 61 AATTCATGAAATATATGATGATGATGATGATGATGATGATGATGATGATGATG 120
Db 61 AATTCATGAAATATATGATGATGATGATGATGATGATGATGATGATGATGATG 120
QY 121 GGAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
Db 121 GGAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
QY 181 GATTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db 181 GATTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
QY 241 AATTCATGAAATATATGATGATGATGATGATGATGATGATGATGATGATGAT 300

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Db 241 AGGCTGAAAGGCTTCTTCAGGCGAAGATGAAGCGAAGGCACTATTACCTGCTCTT 400
QY 301 CAACGGGGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 460
Db 301 CAACGGGGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 460
QY 361 AAGCTGTGTGGACATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
Db 361 AAGCTGTGTGGACATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
QY 421 GAAAGCGGAGATGATGCTGAAAGCGAAGCGAAGCGGCGGCGGCGGCGGCGG 480
Db 421 GAAAGCGGAGATGATGCTGAAAGCGAAGCGAAGCGGCGGCGGCGGCGGCGG 480
QY 481 CAAGCTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 CAAGCTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 CTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db 541 CTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 TGGAGGAGGCGATGCTTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
Db 601 TGGAGGAGGCGATGCTTCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
QY 661 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Db 661 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
QY 721 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
Db 721 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
QY 781 CCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
Db 781 CCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
QY 841 TGGCTTTTGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
Db 841 TGGCTTTTGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
QY 901 GCTGAAGTCAAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 960
Db 901 GCTGAAGTCAAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 960
QY 961 GGAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
Db 961 GGAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
QY 1021 AGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080
Db 1021 AGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1080
QY 1081 GCTGAAGTCAAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1140
Db 1081 GCTGAAGTCAAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1140
QY 1141 TGGCTTTTGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
Db 1141 TGGCTTTTGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
QY 1201 ACTGCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
Db 1201 ACTGCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
QY 1261 GATGATGCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Db 1261 GATGATGCGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 CTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
Db 1321 CTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380

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1056 AGGTCATCAATTTGGCTTCAAGTACAGTCTTACAGTACAGTCTTGGATGATGCTG 1115  
 QY 981 GAAACCAAGACTACAACTACAGGAGGAGTACAGTACAGTAAAGAGAGAGAGAGAG 1040  
 Db 1116 GAAACCAAGACTACAACTACAGGAGGAGTACAGTACAGTAAAGAGAGAGAGAGAG 1175  
 QY 1041 TGATTAGAGGAGGAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAG 1100  
 Db 1176 TGATTAGAGGAGGAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAG 1235  
 QY 1101 AGCAAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1160  
 Db 1236 AGCAAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1295  
 QY 1161 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1220  
 Db 1296 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1355  
 QY 1221 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1280  
 Db 1356 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1415  
 QY 1281 AGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1340  
 Db 1416 AGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1475  
 QY 1341 AGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1399  
 Db 1476 AGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1534

## RESULT 12

AAV03129

ID AAV03129 standard, cDNA, 1960 BP.

XX

AC AAV03129;

XX

XX 11-JUN-1998 (first entry)

XX cDNA encoding rat vitamin D receptor (VDR0).

XX Rat; vitamin D receptor; isoform protein. VDR1, VDR0; diagnosis;

XX dominant negative receptor; signal transmission channel;

XX bone density disorder, screening, ds

XX Rattus rattus.

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A novel cDNA sequence encodes the rat vitamin D receptor isoform protein (VDR1) the isoform differs from the normal receptor (VDR0), which is encoded by the present sequence, in having the vitamin D response element perturbed by 85 residues, and having an extra 19 residues inserted at the C-terminal of this element. It acts as a dominant negative receptor in the vitamin D signal transmission channel.  
 the isoform protein can be used to diagnose bone density disorders, and screen for substances having potential vitamin D-like activity.  
 Sequence 1960 BP: 432 A; 620 C; 457 G; 411 T; 0 other;

Query Match 24.5%; Score 1129.6; DB 19; Length 1960;  
 Requested Similarity: 81.5%; Pred. No. 436 264;  
 Matches 140; Conservative 6; Mismatches 284; Indels 40; Gaps 9;

QY 105 CTCTTCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 164  
 Db 1 CTCTTCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60  
 QY 165 AGCGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 224  
 Db 61 AGCGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120  
 QY 225 ATCTAT 284  
 Db 121 ATCTAT 180  
 QY 285 TATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 344  
 Db 181 TATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
 QY 345 AGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 404  
 Db 241 AGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 400  
 QY 405 ATGAGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 464  
 Db 301 ATGAGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360  
 QY 465 ATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 524  
 Db 361 ATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
 QY 525 AGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 584  
 Db 421 AGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
 QY 585 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 644  
 Db 481 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 528  
 QY 645 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 704  
 Db 529 GCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 588  
 QY 705 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 764  
 Db 589 TGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 648  
 QY 765 TCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 824  
 Db 649 TCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708  
 QY 825 TCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 884  
 Db 709 TCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768  
 QY 885 AGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 944  
 Db 769 AGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 828

DNA encoding a vitamin D receptor isoform protein - useful for bone density determination and for screening substances for vitamin D activity  
 Disclosure: Fig 1; 46pp; Japanese.



[illegible]





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QY 476 CGAGCTAAGATGTTCTCAGAGAGTAGTAGAGGATCATCTGGCATACTGCTGGAGGCGCCACCAT 535
Db 361 CGGCGCAAGATGTTCTCAGAGAGTAGTAGAGGATCATCTGGCATACTGCTGGAGGCGCCACCAT 420
QY 536 AAGACTTACGACCTCCACCTACTCTGGGACTTCTGGGACTTGGGGGCTGGGACTTGGGCTGAAT 595
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QY 1016 ACCAAAGGATGATGCTAGNNNNACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1064
Db 901 ACCAAAGGATGATGCTAGNNNNACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 949
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Search completed: March 2, 2002, 11:17:20  
Job time : 1168 secs



















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1 CLASSIFICATION: 435
2 ALTERNATE/ACRIT INFORMATION:
3 NAME: Lavalley, Jean-Paul M. P.
4 REGISTRATION NUMBER: 41,451
5 REFERENCE/DOCKET NUMBER: 2463-060-55
6 TELECOMMUNICATION INFORMATION:
7 TELEPHONE: (703)521-4500
8 TELEFAX: (703)486-2447
9
10 INFORMATION FOR SEQ ID NO: 5:
11 SEQUENCE CHARACTERISTICS:
12 TYPE: nucleic acid
13 STRANDEDNESS: double
14 TOPOLOGY: linear
15 MOLECULE TYPE: DNA (genomic)
16 ANTI-SENSE: NO
17
18 US-08-696-741-5
19
20 Query Match
21 Best local Similarity 80.9% Score 194.4; DB 1; Length 8174;
22 Mismatches 259; Conservative 0; Mismatches 41; Indels 20; Gaps 2;
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US 09 401 665 4/1\*

1 Sequence No. Application US/09 401 665

2 Patent No. 6206/06

3 GENERAL INFORMATION:

4 APPLICANT: KELLEMS, ROONEY E.

5 APPLICANT: LATA, SURJIT K.

6 APPLICANT: BLAKBORN, MICHAEL R.

7 TITLE OF INVENTION: ADJUSTING DIAMAGNETIC DEFECT DETECTION TRANSDUCER MICE AND

8 FIELD OF INVENTION: METHODS FOR THE USE THEREOF

9 FILE REFERENCES: US/09 401 665

10 CURRENT APPLICATION NUMBER: US/09 401 665

11 CURRENT FILING DATE: 1999-04-28

12 EARLIER APPLICATION NUMBER: 60/083,408

13 EARLIER FILING DATE: 1998-04-29

14 EARLIER APPLICATION NUMBER: 60/083,470

15 EARLIER FILING DATE: 1998-04-28

16 NUMBER OF SEQ. IN NOS: 4

17 SEQUENCE: Patent In Vol. 2,6

18 SEQ. IN NO: 3

19 LENGTH: 46/41

20 TYPE: DNA

21 ORGANISM: Homo Sapiens

22 SEQ. NO: 401 665 4

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GenCore version 5.1.4 p5.4576  
Copyright (c) 1993 - 2002 Compugen Ltd.

on nucleic - nucleic search, using sw model

Run on: March 2, 2003, 14:17:24 ; Search time 279 seconds  
(without alignments)  
10290.827 Million cell updates/sec

Title: US-10-000-213-3

RefSeq score: 4604

Sequence: 1 gaaacacattatcaccacgc.....ataaatctttatgacacac 4564

Scoring table: IDENTITY\_NDP

Gapop 10.0 ; Gapext 1.0

Searched: 46093 seqs, 31899382 residues

Total number of hits satisfying chosen parameters: 921286

Minimum DB seq length: 9

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listed first 45 summaries

Database: Published Applications\_NA:\*

Seq#	Seq Length	Seq ID	Seq Description
1	1025	1025	1025-09-764-877-2904
2	1025	1025	1025-09-764-877-2904
3	1025	1025	1025-09-764-877-2904
4	1025	1025	1025-09-764-877-2904
5	1025	1025	1025-09-764-877-2904
6	1025	1025	1025-09-764-877-2904
7	1025	1025	1025-09-764-877-2904
8	1025	1025	1025-09-764-877-2904
9	1025	1025	1025-09-764-877-2904
10	1025	1025	1025-09-764-877-2904
11	1025	1025	1025-09-764-877-2904
12	1025	1025	1025-09-764-877-2904
13	1025	1025	1025-09-764-877-2904
14	1025	1025	1025-09-764-877-2904

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	565.4	12.3	684	10	US-09-764-877-2904
2	556	7.7	680	10	US-09-764-877-2904
3	280	6.1	292	10	US-09-764-877-2904
4	272.8	5.9	2802	9	US-09-143-828-1
5	272.8	5.9	2905	9	US-09-143-828-1
6	211.2	4.6	473	10	US-09-864-761-6286
7	211	4.6	61814	10	US-09-817-182-1
8	203.2	4.4	9465	9	US-10-092-063-8
9	203.2	4.4	9465	12	US-10-091-085-8
10	199.6	4.3	3453	10	US-09-964-159-1
11	198.4	4.3	75879	10	US-09-854-883-243
12	198.4	4.3	46547	10	US-09-943-267A-1
13	197.6	4.3	291	10	US-09-964-824A-509
14	197.6	4.3	291	10	US-09-965-347-1
15	195.6	4.2	32146	10	US-09-764-860-797
16	195.6	4.2	32248	10	US-09-764-860-802
17	195.6	4.2	468004	10	US-09-949-654-3
18	195.4	4.2	42169	10	US-09-764-847-1963
19	195.2	4.2	155074	9	US-10-025-188-6

Result No.	Score	Query Match	Length	ID	Description
20	194.8	4.2	4963	10	US-09-764-877-2904
21	194.8	4.2	7199	10	US-09-764-869-2279
22	194.6	4.2	543	10	US-09-764-847-1764
23	194.6	4.2	543	10	US-09-764-847-1764
24	194.6	4.2	543	10	US-09-764-847-1767
25	194.6	4.2	5257	10	US-09-908-711-131
26	194.6	4.2	20467	10	US-09-764-877-2725
27	194.6	4.2	20467	10	US-09-764-877-2726
28	194.4	4.2	8174	10	US-09-863-475A-5
29	194.4	4.2	17809	10	US-09-764-847-1133
30	194.4	4.2	36741	10	US-09-782-378A-12
31	194.4	4.2	684973	10	US-09-263-959-1
32	194	4.2	9700	10	US-09-953-342-1
33	194	4.2	17498	10	US-09-764-860-798
34	193.6	4.2	31766	10	US-09-765-344-5
35	193.2	4.2	12452	10	US-09-764-877-4989
36	192.8	4.2	3262	9	US-10-098-841-83
37	192.8	4.2	4037	10	US-09-976-674-40
38	192.8	4.2	4076	10	US-09-976-674-42
39	192.8	4.2	4120	10	US-09-976-674-48
40	192.8	4.2	4159	10	US-09-976-674-40
41	192.8	4.2	4180	10	US-09-976-674-46
42	192.8	4.2	4219	10	US-09-976-674-28
43	192.8	4.2	4263	10	US-09-976-674-44
44	192.8	4.2	4402	10	US-09-976-674-24
45	192.6	4.2	2225	10	US-09-764-878-359

#### ALIGNMENTS

Result No.	Score	Query Match	Length	ID	Description
1	565.4	12.3	684	10	US-09-764-877-2904
2	556	7.7	680	10	US-09-764-877-2904
3	280	6.1	292	10	US-09-764-877-2904
4	272.8	5.9	2802	9	US-09-143-828-1
5	272.8	5.9	2905	9	US-09-143-828-1
6	211.2	4.6	473	10	US-09-864-761-6286
7	211	4.6	61814	10	US-09-817-182-1
8	203.2	4.4	9465	9	US-10-092-063-8
9	203.2	4.4	9465	12	US-10-091-085-8
10	199.6	4.3	3453	10	US-09-964-159-1
11	198.4	4.3	75879	10	US-09-854-883-243
12	198.4	4.3	46547	10	US-09-943-267A-1
13	197.6	4.3	291	10	US-09-964-824A-509
14	197.6	4.3	291	10	US-09-965-347-1
15	195.6	4.2	32146	10	US-09-764-860-797
16	195.6	4.2	32248	10	US-09-764-860-802
17	195.6	4.2	468004	10	US-09-949-654-3
18	195.4	4.2	42169	10	US-09-764-847-1963
19	195.2	4.2	155074	9	US-10-025-188-6

















[illegible]





Genome version 5.1.4.jp6.4578  
Copyright (c) 1993 - 2003 Computer Ltd.

cm nucleic nucleic search, using sw model

Run on: March 2, 2003, 14:02:44 : Search time 5576 seconds

(without alignments)

1586,718 Million cell updates/sec

Title: US-10-000-213-3

Reflected score: 4604

Sequence: 1 gaaacagcttgcacgcgc

Scoring table: 10ENFIX\_N02

Gapop: 10.0 : Gapov: 1.0

Searched: 16154096 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32,608,132

Minimum hit seq length: 0

Maximum hit seq length: 200000000

Post processing: Minimum Match 9%

Maximum Match 100%

Lasting first 45 summaries

Database: 1

EST: \*

1: cm\_est1a: \*

2: cm\_est1b: \*

3: cm\_est1c: \*

4: cm\_est1d: \*

5: cm\_est1e: \*

6: cm\_est1f: \*

7: cm\_est1g: \*

8: cm\_est1h: \*

9: cm\_est1i: \*

10: cm\_est1j: \*

11: cm\_est1k: \*

12: cm\_est1l: \*

13: cm\_est1m: \*

14: cm\_est1n: \*

15: cm\_est1o: \*

16: cm\_est1p: \*

17: cm\_est1q: \*

18: cm\_est1r: \*

19: cm\_est1s: \*

20: cm\_est1t: \*

21: cm\_est1u: \*

22: cm\_est1v: \*

23: cm\_est1w: \*

24: cm\_est1x: \*

25: cm\_est1y: \*

26: cm\_est1z: \*

27: cm\_est1aa: \*

28: cm\_est1ab: \*

29: cm\_est1ac: \*

30: cm\_est1ad: \*

31: cm\_est1ae: \*

32: cm\_est1af: \*

33: cm\_est1ag: \*

34: cm\_est1ah: \*

35: cm\_est1ai: \*

36: cm\_est1aj: \*

37: cm\_est1ak: \*

38: cm\_est1al: \*

39: cm\_est1am: \*

40: cm\_est1an: \*

41: cm\_est1ao: \*

42: cm\_est1ap: \*

43: cm\_est1aq: \*

44: cm\_est1ar: \*

45: cm\_est1as: \*

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	809	17.6	847	9	AU140214	AU140214
2	804	17.4	997	14	BM462824	BM462824
3	786.6	17.1	1048	14	BQ054557	BQ054557
4	743.8	16.2	876	14	BQ281474	BQ281474
5	739.8	16.1	1037	14	BQ067521	BQ067521
6	659.8	14.3	1106	14	BM908433	BM908433

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

C	7	649.8	14.1	725	14	BQ007624
C	8	642.8	14.0	708	10	BE390042
C	9	639.8	13.9	866	13	B1821705
C	10	634.4	13.8	771	10	BE385638
C	11	631.4	13.7	843	9	A1454054
C	12	618.4	13.4	665	10	BE390515
C	13	618.4	13.4	822	9	AA772158
C	14	607.2	13.2	677	14	BE052462
C	15	605.4	13.1	694	9	A1502811
C	16	595	12.9	1051	13	B1656698
C	17	591	12.8	665	9	A1874446
C	18	585.2	12.7	1031	14	BQ671215
C	19	584.8	12.7	622	12	BG149660
C	20	584.6	12.7	556	9	A1923720
C	21	579.8	12.6	687	9	A1989943
C	22	573	12.4	634	9	A1031652
C	23	568.4	12.3	606	13	BM264129
C	24	565.6	12.3	617	9	AA772285
C	25	565.4	12.3	684	9	AA556449
C	26	564.8	12.3	622	14	BQ002808
C	27	559	12.1	594	14	BM764797
C	28	555.4	12.1	612	13	BM264731
C	29	553.6	12.0	687	10	AA057784
C	30	550.8	12.0	618	9	A1458267
C	31	550.8	12.0	625	13	B1823001
C	32	546.8	11.9	584	9	AA855043
C	33	544.6	11.8	584	9	AA706718
C	34	544.6	11.8	618	9	A1055874
C	35	544.6	11.8	682	9	AA648455
C	36	541.8	11.8	579	10	BE676532
C	37	537.4	11.7	577	12	BE661265
C	38	537	11.7	570	14	BM850555
C	39	535	11.6	577	9	A1016571
C	40	533.4	11.6	568	9	A1052108
C	41	530	11.5	554	14	BM745741
C	42	529.8	11.5	554	13	BM127733
C	43	529.8	11.5	562	9	A1949243
C	44	529.8	11.5	562	10	AA874285
C	45	529.4	11.5	554	9	AA723615

## ALIGNMENTS

RESULT 1	AU140214	847 bp	mRNA	linear	EST 05 AUG 2002
LOCUS	AU140214	PLACE2	Homo sapiens	cDNA clone	FLAC2000147 5', mRNA
DEFINITION	AU140214	sequence.			
ACCESSION	AU140214				
VERSION	AU140214.1	GI:11001745			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 847)				
AUTHORS	Ota, T., Suzuki, Y., Saito, K., Ishii, S., Yamamoto, J., Sudiyama, T., Nishikawa, T., Nakamura, Y., Sugano, S., Masuko, Y. and Isotani, T.				
TITLE	HRI human cDNA project (Ota, T., Suzuki, Y., Saito, K., Ishii, S., Yamamoto, J., Sudiyama, T., Nishikawa, T., Nakamura, Y., Sugano, S., Masuko, Y., Isotani, T.)				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Takao Isotani				
	Genomics Laboratory				
	Helix Research Institute				
	1532-3 Yama, Kisarazu, Chiba 292-0812, Japan				
	Tel: 81-438-52-3975				
	Fax: 81-438-52-3986				
	Email: genomics@hri.co.jp				
	HRI: human cDNA project (5' & 3' end overpass sequence)				
	Research Institute: cDNA library construction department of				
	Virology, Institute of Medical Science, University of Tokyo, and				

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Note: "organs": lymph: Vectors: pmt87; Site 1: XhoI; Site 2: EcoR; cDNA made by oligo-dT priming; directionally cloned into EcoR/XhoI sites using the following 5' adaptor: GGACAGG(C). Size selected 500bp for average insert size 1.8kb. Library constructed by Ling Hood in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_Mol. Library."

BASE COUNT	229 a	442 c	270 g	201 t	6 others
ORIGIN					
Query Match	17.1%; Score 786.6; DB 14; Length 1048;				
Best Local Similarity	94.6%; Pred. No. 1.3e-111;				
Matches	883; Conservative 0; Mismatches 50; Indels 10; Gaps 6;				
QY	1570	TTCTGTGGGCTTTTTCGGGCTTGGAGAGCTCAGTCATGAGAGTGTCTGTCTTGTCTT	1629		
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QY	1630	GACAAAGAAACCAATGTGGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1688		
Db	61	GACAAAGAAACCAATGTGGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	120		
QY	1689	TGCTTCACGCTGCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1748		
Db	121	TGCTTCACGCTGCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	180		
QY	1749	CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1808		
Db	181	CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	240		
QY	1809	AGTGGCTAGTGGGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1868		
Db	241	AGTGGCTAGTGGGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	299		
QY	1869	CCAGCCCAACCCCTTCAGTGGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1928		
Db	300	CCAGCCCAACCCCTTCAGTGGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	459		
QY	1929	ATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1988		
Db	360	ATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	419		
QY	1989	GCTGAG	2048		
Db	420	GCTGAG	479		
QY	2049	CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2108		
Db	480	CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	549		
QY	2109	GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2168		
Db	540	GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	599		
QY	2169	CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2228		
Db	600	CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	659		
QY	2229	CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2288		
Db	660	CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	717		
QY	2289	GCAAG	2348		
Db	718	GCAAG	777		
QY	2349	AG	2407		
Db	778	AG	847		
QY	2408	GCAAG	2462		

QY	742	CTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	741		
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QY	742	ATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	791		
Db	481	ATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	540		
QY	792	CTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	851		
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QY	852	ATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	909		
Db	601	ATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	660		
QY	910	ATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	968		
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QY	969	CTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1028		
Db	721	CTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	780		
QY	1029	ATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1087		
Db	781	ATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	840		
QY	1088	CTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1144		
Db	841	CTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	900		
QY	1145	CTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1153		
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FEATURES	<p>DEFINITION: Amino sapiens</p> <p>ACCESSION: B0054557</p> <p>VERSION: B0054557.1</p> <p>KEYWORDS: EST</p> <p>SOURCE: Human</p> <p>ORGANISM: Homo sapiens</p> <p>EXFACILITY: Mammalia: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.</p> <p>NIH Map: http://www.ncbi.nlm.nih.gov/</p> <p>National Institutes of Health, Mammalian Gene Collection (MGC)</p> <p>Unpublished (1999)</p> <p>Contact: Robert Strausberg, Ph.D.</p> <p>Email: rstraus@nsl.nih.gov</p> <p>Tissue Procurement: Lou Staudt</p> <p>cDNA Library Preparation: Rubin Laboratory</p> <p>cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)</p> <p>cDNA Sequenced by: Amersham Bioscience Corporation</p> <p>clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:</p> <p>http://image.llnl.gov</p> <p>High quality sequence stop: 713.</p> <p>Location/Qualifiers</p> <p>1..1048</p> <p>Organization: "Homo sapiens"</p> <p>Gene: "taxid:3456"</p> <p>Feature: "IMAGE:5804841"</p> <p>Feature: "NIH_MGC_99"</p> <p>Feature: "Lymphoma, cell line"</p> <p>Feature: "taxid:3456"</p>				















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TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: eqabps-remail.nih.gov
           Tissue Procurement: ATCC
           cDNA Library Preparation: Ling Hong/Kubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone Distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           plate: LCM254 row: d column: 09
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           Location/Qualifiers
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           /lab_host="DH10B (phage-resistant)"
           /note="Organ: uterus; Vector: pmp7; Site_1: XhoI; Site_2:
           EcoRI; cDNA made by oligo-dT priming. Directionally
           cloned into EcoRI/XhoI sites using the following 5'
           adaptor: GGTAAAG(G). Library constructed by Ling Hong
           in the laboratory of G. Li, M.D., Ph.D., University of
           California, Berkeley) using CAP DNA synthesis kit
           (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 155 a 195 c 170 g 145 t
ORIGIN
Query Match 13 48; Score 618.2; DB 10; Length 665;
Best Local Similarity 98.6%; Pred. No. 1,2e-85;
Matches 655; Conservative 0; Mismatches 6; Indels 3; Gaps 3;
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DB 1 AGGCTGTGTATATGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 60
Q7 421 GAAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
      |||||
DB 61 GAAGCGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
Q7 481 GAAGTGTGTGACATGCGATGATGCAAGAGCTTATTTTACACATGAGCAAGTGTGAGAG 540
      |||||
DB 121 CAAGCTGTGTGACATGCGATGATGCAAGAGCTTATTTTACACATGAGCAAGTGTGAGAG 180
Q7 541 GTATGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
      |||||
DB 181 GTATGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
Q7 601 TTAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
      |||||
DB 241 TTAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
Q7 661 GTGCTGTGTGACATGCGATGATGCAAGAGCTTATTTTACACATGAGCAAGTGTGAGAG 720
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DB 301 GTGCTGTGTGACATGCGATGATGCAAGAGCTTATTTTACACATGAGCAAGTGTGAGAG 360
Q7 721 GTGCTGTGTGACATGCGATGATGCAAGAGCTTATTTTACACATGAGCAAGTGTGAGAG 780
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DB 361 GTGCTGTGTGACATGCGATGATGCAAGAGCTTATTTTACACATGAGCAAGTGTGAGAG 420
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Q7 840 GTGCTGTGTGACATGCGATGATGCAAGAGCTTATTTTACACATGAGCAAGTGTGAGAG 899
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DB 541 TGTCTAAGTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
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DB 661 GCAA 664
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AA772158
DEFINITION aa772158.1 Soares_parathyroid_tumor_NBHPA Homo sapiens cDNA clone
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ACCESSION AA772158
VERSION AA772158.1 GI:2823941
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 822)
AUTHORS M. Soares, R. Strausberg, G. Li, Ph.D., a biologist,
           National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
           Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
           Email: eqabps-remail.nih.gov
           cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Ronaldo
           , Ph.D.
           cDNA Library Arrayed by: Greg Lennon, Ph.D.
           DNA Sequencing by: Washington University Genome Sequencing Center
           Clone Distribution: NCI-CGAP clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
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           /dev_stage="adult"
           /lab_host="DH10B (ampicillin resistant)"
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           primer.
           [5'-TGTTACCAATCTCAATGCGAGCGCGGCCACCAATTTTCTTTTCTTTTCTTTT
           TTTT 3'], double stranded cDNA was size selected, ligated
           to Eco RI adapters (Pharmacia), digested with Not I and
           cloned into the Not I and Eco RI sites of a modified pT73
           vector (Pharmacia). Library went through one round of
           normalization to a cat 5' library constructed by Bento
           Soares and M. Fatima Ronaldo. RNA from sporadic parathyroid
           adenomas was kindly provided by Dr. Stephen Marx, Rational
           Institute of Diabetes and Digestive and Kidney Diseases,
           NIH."
BASE COUNT 194 a 188 c 180 g 260 t
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Query Match 13 48; Score 610.2; DB 9; Length 822;
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QY 4424 GGCAGCGAAGGATGTAACACAGCTGCTCTCTGATGATTCCTAAAGGAAAAAAGAGTTGCG 4483
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QY 4484 CAGACATTTCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 4543
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Db 77 TATTATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 19

RESULT 15
A1302811.1 694 bp mRNA linear EST 01-FEB-1999
LOCUS A1302811.1
DEFINITION q55g07 xl N1-CCAP_Kid5 Homo sapiens cDNA clone (IMAGE:156249)
similar to gb:J03258 VITAMIN D3 RECEPTOR (HUMAN); mRNA sequence.
ACCESSION A1302811
VERSION 1
KEYWORDS EST
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 694)
AUTHORS NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap/
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: eqabp@mail.nih.gov
Tissue Procurement: Christopher Miskaik, M.D., Ph.D., Michael R
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CCAP clone distribution information can be
found through the I M A G E Consortium/IMG at:
www.bio.illinois.gov/bbyp/image/image.html
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Seq primer: -400P from Gibco
High quality sequence stop: 464.
Location/Qualifiers
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/label="DH10R"
/notes="organ: Kidney; Vector: pTZ19-pac (Pharmacia) with
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AACGGGAAGATCGGCGCGCAATTTTTTTTTTTTTTTT 3').
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not 1 and cloned into the Not 1
and Eco RI sites of the modified pTZ19 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 176 a 162 c 136 g 219 t 1 others
ORIGIN
Query Match 13.1%; Score 605.4; DB 9; Length 694;
Best Local Similarity 96.2%; Pred. No. 1.1e-83;
Matches 662; Conservative 0; Mismatches 22; Indels 4; Gaps 4;
QY 4919 CCCCACACATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3978
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Db 693 CAGCGAAGGATGTAACACAGCTGCTCTCTGATGATTCCTAAAGGAAAAAAGAGTTGCG 645
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QY 4979 GGCAGCGAAGGATGTAACACAGCTGCTCTCTGATGATTCCTAAAGGAAAAAAGAGTTGCG 4038
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Search completed: March 2, 2003, 18:54:54  
Job time : 5605 secs

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Db 634 GGCAGCGAAGGATGTAACACAGCTGCTCTCTGATGATTCCTAAAGGAAAAAAGAGTTGCG 575
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Db 574 GGCAGCGAAGGATGTAACACAGCTGCTCTCTGATGATTCCTAAAGGAAAAAAGAGTTGCG 515
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QY 4097 GGCAGCGAAGGATGTAACACAGCTGCTCTCTGATGATTCCTAAAGGAAAAAAGAGTTGCG 4156
|||||
Db 514 GGCAGCGAAGGATGTAACACAGCTGCTCTCTGATGATTCCTAAAGGAAAAAAGAGTTGCG 455
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QY 4157 GGCAGCGAAGGATGTAACACAGCTGCTCTCTGATGATTCCTAAAGGAAAAAAGAGTTGCG 4216
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|||||
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|||||
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|||||
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|||||
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